

~~10/537000~~ 10/538/000

WO 2004/030468

PCT/EP2003/014553

1/4

JC20 Rec'd PCT/PTO D9 JUN 2005

SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> NOVEL FOOD PRODUCTION PROCESS

<130> 21401WO

<160> 3

<170> PatentIn version 3.1

<210> 1

<211> 3223

<212> DNA

<213> Aspergillus niger

<400> 1

tggggggaaac ttgcatactga	gagcatcata	ctagttacta	ctactactac	tacttgccga	60
tgaataaaca tcctgcttgt	actacgcata	gccgtcttgc	tgacatggag	atataattttg	120
ggctccgaga gtttgatag	cagtagccaa	ttaactagta	gatgcttagta	ctactctagt	180
aatttggggg cgaatgttga	atccagctca	tgccaaattga	catactggaga	tctccacgag	240
acaacgagat aagatgaaat	attgctgtca	tgggtgataa	ctagatgttt	cgagaaggat	300
tcttgaggat tgccatcatcg	catggataa	tatcaccctc	gggtggacat	tcccggctgt	360
tggggcttat cgttgaagag	tcaccccccga	tatcgggtgg	ccaaggccctt	tatcaatcat	420
catcctatca gtttccaccc	acaagatagc	ctatggaccc	tgtatccctt	ctagccacag	480
agactagtagc tagtctatca	tgtcgactcc	atgtggagaa	accctgtataa	gaccatgtgg	540
aggaggagat agcaagcctc	cacagaaaca	atatcatctc	cacctgcaat	cacggttgg	600
ttccgaatac acccgccgcc	tggcaagcac	atgggttata	aatgtctgaa	accaggcaag	660
atgaatttgg aagagaagcca	gcagagacca	tcgcataccgt	tttcatcatg	cctctcaagc	720
cgattctcct gtcgtccctg	gccagtcctc	cctccggctc	tccgctgctc	tactcgccga	780
ccaccaatga aacccctgctc	ttcaccatgc	ccaatggcct	caacttcacc	cagatgaaca	840
ccaccctgcc gAACGTGACC	attttgcctt	cggttaggtg	gaccgagttat	acctcaggta	900
gtgcgaccga tagtttaccg	caactcacag	gtgttaccat	cgccgggttcc	gattccagct	960
caaccggccac gaccggctac	acctccggag	cagtcggggt	cctgtccctc	atcgatgcgg	1020
tgccatccat gttggatgtt	gccaatgtt	ccggcgttcc	gttggcaac	gtggaaagcg	1080
aggatatcac ctctgacatc	ctgatccatc	tgtccaagaa	gctgaaccgc	gttgtatgt	1140
aggacccgac catggccgtt	gctgtcatca	cccacggcac	cgacaccctc	gaggagactg	1200
ccttcttccct ggacgcaact	gtcaactgtt	gcaagccaaat	tgtcatcggt	gttgccatgc	1260
gccccatccac ggcacatctca	gctgacgggc	ccttcaatct	gctcgaagcc	gtgacgggt	1320
ctgcctccac gtcggcgcgc	gatcgcgtt	ccatgggtgt	catgaacgat	cgcatggcct	1380
cgccctacta tgtgaccaag	accaatgcca	acactatgg	cacccatcaag	gcatggaga	1440
tgggcttaccc tggcgagatg	atctccaaaca	cccccttctt	tttcttaccc	ccccgtcaagc	1500
caacccggtaa ggtggccctt	gacatcacca	acgtgactga	gatccccctgt	gtggacattc	1560
tgttttctta tgaggacatg	cacaacgaca	ccctctacaa	cgccatctcc	agtgggtccc	1620
agggaaattgt ggtgagttgt	atttcccttgc	tctctctcta	aaaaacttgg	aatggacgct	1680
gatgagaata gattggccgg	gctgggtctg	gaggcgtcac	acactcccttc	aatgaggcta	1740
tcgaggatgt catcaaccgt	ttggagatcc	ctgtcggtca	gagttatgcgc	acagtcaatg	1800
gggaagtgcc acttgcac	gtgagcagcg	acaccggccac	ccacatcgcc	agtggatacc	1860
taaaccggca gaagtccgc	atctgttgg	gattgtctgt	atcccaggga	aagaatata	1920
ccgaaatccgc tgacgtgtt	gctctgggca	cggtatgcgt	gttgcgtat	gaaccattgt	1980
atataataat gaccggatat	tatgtatcat	atagatttgc	atagaaatgt	actggataca	2040
catcagcaaa ggataccgag	ttttggccctc	aggcggttgc	agaaaaatgt	tatccactg	2100
aagatcatga atcatgttt	atcttctggc	ccccctcgat	ccagggtgtt	ggacatgcag	2160
ggtgcttgc gtctgaagga	tccgagatca	aatttgcac	agccagagtc	tgatacatcc	2220
ataatagtgg gtatatttga	agtccattga	tagtccctgt	ttgtgtcggtt	caattgggtt	2280

agcttagggcc tggcttggtg	gcatatcg	ttt	ggactaatag atggtagttc	aattaccgac	2340
ggactgtct cccgcatt	tttcacaa	ttt	ttttcagc acat	tttgcgtt	2400
ggatctgcaa tatttttc	cctcgcatc	ttt	ttttccac gaaaagacca	tccagacatc	2460
ttgctcgta ttctggacc	taagactgtt	ttt	ttgaaaaggca aatgtaaaagc	gtgattggtc	2520
gacgtcaagc ctgaccaatc	tagtaagctg	gtt	gtttacttt ggggttagac	ggaggattta	2580
ggtagtatta aggca	ggcagctag	ttc	ggcctgc ttaccacca	ggcgaggcac	2640
atcaggcg	aaatggaa	ccg	aagtgcgagg tccacttaac	atgatgcgcg	2700
ggcgaccaag accctggatt	gatcgctatg	att	cccgccggat tttcacggc	ccctgaaggg	2760
tttcgataac gcaggattgg	atccctccag	cctcgctct	gcaagtggaa	2820	
ctctccgtca cgtcattact	cagacactcc	cat	tttgc ttat	tgaatcttat	2880
gggctgaccc tcagctcg	gtgggatg	cc	tgaatcg	gtgaaagtctt	2940
tcctagcc	ctggtagagg	cg	gatgat	taataatcaa	3000
aaggctgtc cctggtcaac	catcactctg	gtt	tttgc gttt	gggagacagc	3060
tgaagccat tgcggt	taat	gtt	tttgc	gagtca	3120
agaccgggtt tcgcacgg	gcagaaccgc	atccaa	acgc	tttgc	3180
ggatactcat ccgtctatt	tg	tttgc	tttgc	tttgc	3223

<210> 2
 <211> 1137
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> CDS
 <222> (1)...(1137)

<400> 2			
atg cct ctc aag ccg att ctc ctg tct gcc ctg	gcc agt ctc	gcc tcg	48
Met Pro Leu Lys Pro Ile Leu Leu Ser Ala	Leu Ala Ser Leu Ala Ser		
1 5 10 15			
gcc tct ccg ctg ctc tac tcg	cg acc acc aat	gaa acc ttc gtc ttc	96
Ala Ser Pro Leu Leu Tyr Ser Arg Thr	Thr Asn Glu Thr Phe Val Phe		
20 25 30			
acc aat gcc aat ggc ctc aac ttc acc	cag atg aac acc acc	ctg ccg	144
Thr Asn Ala Asn Gly Leu Asn Phe	Thr Gln Met Asn Thr	Thr Leu Pro	
35 40 45			
aac gtg acc att ttc gca acg	ggt ggt acc atc	gcc ggc tcc gat tcc	192
Asn Val Thr Ile Phe Ala Thr	Gly Gly Thr Ile Ala	Gly Ser Asp Ser	
50 55 60			
agc tca acc gcc acg acc ggc tac	acc tcc gga gca gtc	ggg gtc ctg	240
Ser Ser Thr Ala Thr	Gly Tyr Thr Ser	Gly Ala Val Gly Val Ieu	
65 70 75 80			
tcc ctc atc gat gcg	gtg cca tcc atg	ctg gat gtg	288
Ser Leu Ile Asp Ala Val Pro Ser	Met Leu Asp Val	Ala Asn Val Ala	
85 90 95			
ggc gtc cag gtg	gcc aac gtg	gga agc gag	336
Gly Val Gln Val Ala Asn Val	Gly Ser Glu Asp Ile	Thr Ser Asp Ile	
100 105 110			
ctg att tcc atg	tcc aag aag	ctg aac cgc	384
Leu Ile Ser Met Ser	Lys Lys Leu Asn Arg	Val Val Cys Glu Asp Pro	
115 120 125			
acc atg gcc ggt	gct gtc atc	acc cac ggc acc	432
Thr Met Ala Gly Ala Val Ile	Thr His Gly Thr Asp	Thr Leu Glu Glu	
130 135 140			
act gcc ttc ttc ctg	gac gcc act	gtc aac tgt	480
Thr Ala Phe Phe Leu Asp Ala	Thr Val Asn Cys	Gly Lys Pro Ile Val	

<210> 3
<211> 378
<212> PRT
<213> *Aspergillus niger*

<400> 3
 Met Pro Leu Lys Pro Ile Leu Leu Ser Ala Leu Ala Ser Leu Ala Ser
 1 5 10 15
 Ala Ser Pro Leu Leu Tyr Ser Arg Thr Thr Asn Glu Thr Phe Val Phe
 20 25 30
 Thr Asn Ala Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro
 35 40 45

Asn Val Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Asp Ser.
50 55 60
Ser Ser Thr Ala Thr Thr Gly Tyr Thr Ser Gly Ala Val Gly Val Leu
65 70 75 80
Ser Leu Ile Asp Ala Val Pro Ser Met Leu Asp Val Ala Asn Val Ala
85 90 95
Gly Val Gln Val Ala Asn Val Gly Ser Glu Asp Ile Thr Ser Asp Ile
100 105 110
Leu Ile Ser Met Ser Lys Lys Leu Asn Arg Val Val Cys Glu Asp Pro
115 120 125
Thr Met Ala Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
130 135 140
Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
145 150 155 160
Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
165 170 175
Phe Asn Leu Leu Glu Ala Val Thr Val Ala Ala Ser Thr Ser Ala Arg
180 185 190
Asp Arg Gly Ala Met Val Val Met Asn Asp Arg Ile Ala Ser Ala Tyr
195 200 205
Tyr Val Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Met
210 215 220
Glu Met Gly Tyr Leu Gly Glu Met Ile Ser Asn Thr Pro Phe Phe Phe
225 230 235 240
Tyr Pro Pro Val Lys Pro Thr Gly Lys Val Ala Phe Asp Ile Thr Asn
245 250 255
Val Thr Glu Ile Pro Arg Val Asp Ile Leu Phe Ser Tyr Glu Asp Met
260 265 270
His Asn Asp Thr Leu Tyr Asn Ala Ile Ser Ser Gly Ala Gln Gly Ile
275 280 285
Val Ile Ala Gly Ala Gly Gly Val Thr Thr Ser Phe Asn Glu
290 295 300
Ala Ile Glu Asp Val Ile Asn Arg Leu Glu Ile Pro Val Val Gln Ser
305 310 315 320
Met Arg Thr Val Asn Gly Glu Val Pro Leu Ser Asp Val Ser Ser Asp
325 330 335
Thr Ala Thr His Ile Ala Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg
340 345 350
Ile Leu Leu Gly Leu Leu Ser Gln Gly Lys Asn Ile Thr Glu Ile
355 360 365
Ala Asp Val Phe Ala Leu Gly Thr Asp Ala
370 375